

Package: walk (via r-universe)

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Title Model Animal Movement With Continuous-Time Markov Chains

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Description Model animal movement using continuous-time Markov chain models.

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Imports TMB (>= 1.9.0), Matrix, terra, dplyr, mvtnorm, numDeriv, optimx, sf, spdep, ctmm, methods, tidyR, rARPACK

LinkingTo TMB, Rcpp, RcppArmadillo, expQ2

Remotes dsjohnson/expQ2

NeedsCompilation yes

Depends R (>= 2.10)

LazyData true

Config/pak/sysreqs cmake libgdal-dev gdal-bin libgeos-dev libgmp3-dev libgsdl0-dev libicu-dev libmpfr-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev

Repository <https://dsjohnson.r-universe.dev>

RemoteUrl <https://github.com/dsjohnson/walk>

RemoteRef HEAD

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arg_funcs*Define specifics for model structure and fitting control*

Description

Define specifics for model structure and fitting control

Usage

```
ctmc_model(form = ~1, link = "soft_plus", a = 1, L = 0, U = 0)

ctmc_control(
  q_r = ctmc_model(),
  q_m = ctmc_model(),
  p = FALSE,
  delta = "uniform",
  form = "mult",
  norm = TRUE
)
```

Arguments

- form** The form of the rate matrix entries. Can be one of: "mult" for residency times movement, i.e., $q_{ij} = q_r(i) * \pi_m(i,j)$, "add" for a model of the form $q_{ij} = q_r(i) + \pi_m(i,j)$, and "sde" for a Langevin diffusion approximation. The "sde" is very similar to the additive model.
- link** A link function for the residency or movement model. One of "soft_plus" or "log".
- a** Scale parameter for the "soft_plus" link function. Ignored for link="log". The a parameter determines the approximation to a hard plus function, i.e., as a becomes large the soft plus function converges to $g^{-1}(x) = \max(0, x)$. For this specification, a must be greater than or equal to 1.
- q_r** A named list for the residency model. Must contain elements: form, link, and a. The easiest way to construct this is the ctmc_model function.
- q_m** A named list for the movement portion of the model. See q_r.

p	Logical. Should a zero-inflation parameter be used. Necessary when there might be outliers when the location likelihood does not overlap likely locations.
delta	Vector of probabilities for the initial location. Can be one of "uniform" for a uniform distribution over all cells, "stationary" to use the stationary distribution implied by the parameters, or a numeric vector the same length as the number of cells.
norm	Should the movement portion be adjusted to sum to 1. This is the parameterization suggested by Hewitt et al. (2023).

References

Hewitt, J., Gelfand, A. E., & Schick, R. S. (2023). Time-discretization approximation enriches continuous-time discrete-space models for animal movement. *The Annals of Applied Statistics*, 17:740-760.

ctmc_n2ll

Evaluate movement MMPP log-likelihood

Description

Evaluate movement MMPP log-likelihood

Usage

```
ctmc_n2ll(par, data_list, check_rho = NULL, debug = 0, ...)
```

Arguments

par	Parameter vector
data_list	List of required data objects to evaluate likelihood
check_rho	Check if rho is too big for uniformitazation calculation of expQ. Value is the size of rho to check.
debug	For developers only, leave in the default setting.
...	Extra wiggle room for ignored arguments.

Author(s)

Devin S. Johnson

dm_matrix	<i>Create sparse representations of design matrices for movement and resight models</i>
-----------	---

Description

Create sparse representations of design matrices for movement and resight models

Usage

```
dm_q_m(formula, ddl)
```

```
dm_q_r(formula, ddl)
```

Arguments

- | | |
|---------|---|
| formula | An R formula object for the parameter vector. |
| ddl | Design data list |

Details

This function is not designed for end-users but is exported for posterity.

fit_ctmc	<i>Fit CTMC movement model to telemetry data</i>
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Description

Fit CTMC movement model to telemetry data

Usage

```
fit_ctmc(
  walk_data,
  model_parameters = ctmc_control(),
  pen_fun = NULL,
  hessian = TRUE,
  reals = FALSE,
  start = NULL,
  method = "nlminb",
  fit = TRUE,
  eq_prec = 1e-08,
  check_rho = NULL,
  debug = 0,
  ...
)
```

Arguments

<code>walk_data</code>	A design data list produced by the function make_walk_data .
<code>model_parameters</code>	A named list giving specifications for the model. See ctmc_control .
<code>pen_fun</code>	An optional penalty function. Should be on the scale of a log-prior distribution.
<code>hessian</code>	Logical. Should the Hessian matrix be calculated to obtain the parameter variance-covariance matrix.
<code>reals</code>	Calculate real values for expected residency, cell transition probabilities, and outlier proportion for observations.
<code>start</code>	Optional starting values for the parameter must be a list of the form <code>list(beta_l=c(), beta_q_r=c(), beta_q_r=c())</code> .
<code>method</code>	Optimization method. See optimr
<code>fit</code>	Logical. Should the likelihood be optimized?
<code>eq_prec</code>	Error rate of matrix exponential calculation. Defaults to <code>1.0e-8</code> . This is a generous value. If the model is running slow, you can try reducing it to, say, <code>1.0e-4</code> .
<code>check_rho</code>	Check if rho is too big for uniformitzation calculation of <code>expQt</code> . Value is the size for which rho is too big, causing likelihood calculation error.
<code>debug</code>	Integer from 1-4. Opens browser() at various points in the function call. Mostly for package developers.
<code>...</code>	Additional arguments passed to the optimization function optimr from the optimx-package .

Author(s)

Devin S. Johnson

`gen_invLogit` *General inverse logit function*

Description

General inverse logit function

Usage

```
gen_invLogit(x, L = 0, U = 1)
```

Arguments

<code>x</code>	numeric value
<code>L</code>	Lower bound
<code>U</code>	Upper bound

<code>get_betas</code>	<i>Summarize beta parameter values</i>
------------------------	--

Description

Takes fitted model and produces a summary of the beta estimates.

Usage

```
get_betas(par, V = NULL, data_list)
```

Arguments

<code>par</code>	Model estimated parameters
<code>V</code>	Optional variance-covariance matrix for the parameters. If none is given no standard errors will be provided for the real parameter estimates
<code>data_list</code>	The data list from a fitted model object

Author(s)

Devin S. Johnson

<code>get_lim_ud</code>	<i>Get the limiting utilization distribution of the CTMC movement process</i>
-------------------------	---

Description

Get the limiting utilization distribution of the CTMC movement process

Usage

```
get_lim_ud(fit = NULL, hpd = NULL, method = "lu", ...)
```

Arguments

<code>fit</code>	A moveMMPP fitted model object from fit_mmpp_dir .
<code>hpd</code>	A vector of probabilities. Will return columns with highest probability area for each specified probability. E.g., <code>hpd=c(0.5, 0.95)</code> will return 2 extra columns with 50 and 95% HPD densities.
<code>method</code>	Method used for eigen decomposition. One of "lu" or "arpack".
...	Extra arguments to pass to <code>eigs</code>

Author(s)

Devin S. Johnson

get_Q*Get movement transition matrix from fitted moveMMP object*

Description

Get movement transition matrix from fitted moveMMP object

Usage

```
get_Q(fit, sparse = TRUE)
```

Arguments

- | | |
|--------|---|
| fit | A moveMMPP fitted model object from fit_mmpp_dir . |
| sparse | Logical. Should the matrix be returned in a sparse format from the Matrix package. Defaults to sparse = TRUE. |

Author(s)

Devin S. Johnson

make_walk_data*Produce design data for use in fitting MMPP movement models*

Description

Produce design data for use in fitting MMPP movement models

Usage

```
make_walk_data(  
  proc_data,  
  cell_data,  
  grad = NULL,  
  rast_mask = NULL,  
  directions = "rook",  
  debug = 0,  
  ...  
)
```

Arguments

<code>proc_data</code>	A sparse matrix with rows corresponding to time steps and columns corresponding to cells. The entries are probabilities that the animal is located in the corresponding cell and time.
<code>cell_data</code>	A SpatRaster object from the terra package.
<code>grad</code>	A character vector of names of <code>cell_data</code> layers for which gradient covariates will be constructed.
<code>rast_mask</code>	Raster mask for inaccessible cells when <code>cell_data</code> is of type SpatRaster from the terra package. This is ignored if <code>cell_data</code> is an POLYGON data frame from the sf package.
<code>directions</code>	—.
<code>debug</code>	Debugging level: 1-3 mainly for package developers.
...	Ignored arguments.

`predict_ctmc`*Predict Movement Path From Fitted CTMC Model***Description**

Predict Movement Path From Fitted CTMC Model

Usage

```
predict_ctmc(
  fit,
  walk_data,
  aux_timestamp = NULL,
  trunc_tol = 1e-08,
  debug = 0,
  ...
)
```

Arguments

<code>fit</code>	A fitted model object produced by fit_ctmc
<code>walk_data</code>	A design data list produced by the function make_walk_data .
<code>aux_timestamp</code>	Additional POSIX times for which location prediction is desired.
<code>trunc_tol</code>	Level for truncating small location prediction probabilities.
<code>debug</code>	Developer debugging.
...	Aditonal arguments passed to internal function <code>ctmc_predict_arma</code> .

Author(s)

Devin S. Johnson

References

Hewitt, J., Gelfand, A. E., & Schick, R. S. (2023). Time-discretization approximation enriches continuous-time discrete-space models for animal movement. *The Annals of Applied Statistics*, 17:740-760.

proc_telem

Convert ctmm telemetry data object to a terra SpatRaster stack

Description

Convert ctmm telemetry data object to a terra SpatRaster stack

Usage

```
proc_telem(  
  data,  
  cell_data,  
  time_unit = "hours",  
  return_type = "sparse",  
  max_err = NULL,  
  trunc = 1e-08  
)
```

Arguments

data	A telemetry object from the ctmm package
cell_data	A \link[terra]{SpatRaster} stack of covariates that will be used in CTMC movement modeling. Cells with NA values will be considered areas to the animal cannot travel, i.e., likelihood surfaces will be 0 for those cells.
time_unit	Unit of measurement for numeric conversion of the POSIX timestamps in the telemetry data. Defaults to "hours". Can specify, e.g., "seconds" or "days"
return_type	Type of object returned. One if "data.frame", "sparse" (sparse matrix), "matrix_df" (matrix form of "data.frame"), or "dense" (dense matrix).
max_err	The maximum error in meters. If unspecified it will be set to 4 times the maximum error standard deviation as determined by the UERE and HDOP of the telemetry data.
trunc	The smallest probability value that is considered to be > 0. Defaults to 1.0e-8.

Details

This function takes the HDOP information in the telemetry object to produce a SpatRaster like-likelihood surface over the SpatRaster defined by the raster argument for each location. This can then be passed to CTMC HMM fitting functions.

Author(s)

Devin S. Johnson

`set_barrier_mask` *Denote cells where the animal cannot travel*

Description

Denote cells where the animal cannot travel

Usage

```
set_barrier_mask(x, y, overlap = 0.95)
```

Arguments

<code>x</code>	a polygon object that denotes places where the animal cannot travel
<code>y</code>	A SpatRaster where cells will be set to NA that are inside the polygon object.
<code>overlap</code>	The amount of overlap between the raster cell and polygon such that the cell is considered "inside" the polygon. Defaults to <code>overlap = 0.95</code> . If <code>overlap = 1</code> then a cell has to be completely inside the polygon to be masked.

`softPlus` *Soft-plus function*

Description

Soft-plus function

Usage

```
softPlus(x, a = 1)
```

Arguments

<code>x</code>	numeric value
<code>a</code>	scale parameter, a must be >1.

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